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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2007; month=12; day=20; hr=11; min=45; sec=45; ms=947;
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Application No: 10578615 Version No: 1.0

Input Set:

Output Set:

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Finished: 2007-12-20 11:22:51.814
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 2 ms
Total Warnings: 22
Total Errors: 0
No. of SeqIDs Defined: 22
Actual SeqID Count: 22

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (18)
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W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

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Error code	Error Description
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<110> Tohata, Masatoshi
Sawada, Kazuhisa
Ozaki, Katsuya
Sekiguchi, Junichi

<120> RECOMBINANT MICROORGANISM

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Lys Gln Leu Ile Ser Ser Ile Leu Ile Leu Val Leu Leu Ser Leu	
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 ttt ccg gca gct ctt gca gca gaa gga aac act cgt gaa gac aat ttt	689
Phe Pro Ala Ala Leu Ala Glu Gly Asn Thr Arg Glu Asp Asn Phe	
25 30 35	
 aaa cat tta tta ggt aat gac aat gtt aaa cgc cct tct gag gct ggc	737
Lys His Leu Leu Gly Asn Asn Val Lys Arg Pro Ser Glu Ala Gly	
40 45 50 55	
 gca tta caa tta caa gaa gtc gat gga caa atg aca tta gta gat caa	785
Ala Leu Gln Leu Gln Glu Val Asp Gly Gln Met Thr Leu Val Asp Gln	
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 cat gga gaa aaa att caa tta cgt gga atg agt aca cac gga tta cag	833
His Gly Glu Lys Ile Gln Leu Arg Gly Met Ser Thr His Gly Leu Gln	
75 80 85	
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Trp Phe Pro Glu Ile Leu Asn Asp Asn Ala Tyr Lys Ala Leu Ser Asn	
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Asp Trp Asp Ser Asn Met Ile Arg Leu Ala Met Tyr Val Gly Glu Asn	
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Gly Tyr Ala Thr Asn Pro Glu Leu Ile Lys Gln Arg Val Ile Asp Gly	
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Ile Glu Leu Ala Ile Glu Asn Asp Met Tyr Val Ile Val Asp Trp His	
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Val His Ala Pro Gly Asp Pro Arg Asp Pro Val Tyr Ala Gly Ala Lys	
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Asp Phe Phe Arg Glu Ile Ala Ala Leu Tyr Pro Asn Asn Pro His Ile	
170 175 180	
 att tat gag tta gcg aat gag ccg agt agt aat aat aat ggt gga gca	1169
Ile Tyr Glu Leu Ala Asn Glu Pro Ser Ser Asn Asn Gly Gly Ala	
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Gly Ile Pro Asn Asn Glu Glu Gly Trp Lys Ala Val Lys Glu Tyr Ala	
200 205 210 215	

gat cca att gta gaa atg tta cgt aaa agc ggt aat gca gat gac aac			1265
Asp Pro Ile Val Glu Met Leu Arg Lys Ser Gly Asn Ala Asp Asp Asn			
220	225	230	
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Ile Ile Ile Val Gly Ser Pro Asn Trp Ser Gln Arg Pro Asp Leu Ala			
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Ala Asp Asn Pro Ile Asp Asp His His Thr Met Tyr Thr Val His Phe			
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Tyr Thr Gly Ser His Ala Ala Ser Thr Glu Ser Tyr Pro Ser Glu Thr			
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cct aac tct gaa aga gga aac gta atg agt aac act cgt tat gcg tta			1457
Pro Asn Ser Glu Arg Gly Asn Val Met Ser Asn Thr Arg Tyr Ala Leu			
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Glu Asn Gly Val Ala Val Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala			
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agt gga gac ggt ggt cct tac ttt gat gaa gca gat gta tgg att gaa			1553
Ser Gly Asp Gly Pro Tyr Phe Asp Glu Ala Asp Val Trp Ile Glu			
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Phe Leu Asn Glu Asn Asn Ile Ser Trp Ala Asn Trp Ser Leu Thr Asn			
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Lys Asn Glu Val Ser Gly Ala Phe Thr Pro Phe Glu Leu Gly Lys Ser			
345	350	355	
aac gca acc aat ctt gac cca ggt cca gat cat gtg tgg gca cca gaa			1697
Asn Ala Thr Asn Leu Asp Pro Gly Pro Asp His Val Trp Ala Pro Glu			
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Asn Tyr Glu Pro Ile Asp Arg Thr Lys Tyr Thr Lys Val Leu Trp Asp			
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Phe Asn Asp Gly Thr Lys Gln Gly Phe Gly Val Asn Ser Asp Ser Pro			
410	415	420	
aat aaa gaa ctt att gca gtt gat aat gaa aac aac act ttg aaa gtt			1889
Asn Lys Glu Leu Ile Ala Val Asp Asn Glu Asn Asn Thr Leu Lys Val			
425	430	435	
tcg gga tta gat gta agt aac gat gtt tca gat ggc aac ttc tgg gct			1937

Ser Gly Leu Asp Val Ser Asn Asp Val Ser Asp Gly Asn Phe Trp Ala
 440 445 450 455
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 Asn Ala Arg Leu Ser Ala Asn Gly Trp Gly Lys Ser Val Asp Ile Leu
 460 465 470
 1985
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 Gly Ala Glu Lys Leu Thr Met Asp Val Ile Val Asp Glu Pro Thr Thr
 475 480 485
 2033
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 Val Ala Ile Ala Ala Ile Pro Gln Ser Ser Lys Ser Gly Trp Ala Asn
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 Gln Gly Trp Asp Trp Ala Gly Glu Ser Gly Val Lys Thr Ala Leu Thr
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665 670 675

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700 705 710

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715 720 725

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760 765 770 775

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Pro Gly Glu Glu Thr Pro Pro Val Asp Glu Lys Glu Ala Lys Lys Glu
780 785 790

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Gln Lys Glu Ala Glu Lys Glu Glu Lys Glu Ala Val Lys Glu Glu Lys
795 800 805

aaa gaa gct aaa gaa gaa aag aaa gca gtc aaa aat gag gct aag aaa 3041
Lys Glu Ala Lys Glu Glu Lys Lys Ala Val Lys Asn Glu Ala Lys Lys
810 815 820

aaa taatctatta aactagttat agggtttatct aaaggctctga tgttagatctt 3094
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25

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Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln Leu Arg Gly
65 70 75 80

Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu Asn Asp Asn
85 90 95

Ala Tyr Lys Ala Leu Ser Asn Asp Trp Asp Ser Asn Met Ile Arg Leu
100 105 110

Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Thr Asn Pro Glu Leu Ile
115 120 125

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Pro Val Tyr Ala Gly Ala Lys Asp Phe Phe Arg Glu Ile Ala Ala Leu
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195 200 205

Lys Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met Leu Arg Lys
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Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser Pro Asn Trp
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Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp Asp His His
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Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala Ala Ser Thr
260 265 270

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515 520 525

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